

Figure 1A

TrpGGGGACAGCCCCCCACCATTCCTACCGCTATGGGCCCCAACCTCCCACTCC CACCTCCCTCCATCGGCCGGGCTAGGACACCCCCAAATCCCGTCGCCC GCA TGG CCGCTGCCGCAGCCTGGCGGGGGGGGCCAGCCCCCCAGGCCCCCTAC CCTTGGCACCGACACCCGACAGAGACAGAGACACAGCCATCCGCCACCA GGAAGTCAGCAGGCGTTGGGGAGGGGTGGCGGGGGAATAGCGGCGGCAGC Pro Gly Ala CCA GGG Trp TGG Leu TTG Asp GAT Met ATG CCCTCTGAGGTGGCCAGA 101 51 01 51 301

Replacement Sheet
Appl. No.: 10/667,494
Title: HUMAN LYSOPHOSPHATIDIC ACID
ACYLTRANSFERASE GAMMA-1

POLYPEPTIDE (As Amended) Inventors: David W. LEUNG et al. Atty. Docket No.: 077319-0381

> 20 П CCC AGT GCC AAG Phe Len Len Leu Leu Phe Leu Leu Leu Leu Leu Met

CTG CTG CTC TTC C

CTG

TTC

CTC

CTG

CTG

CTG

CTG

ATG

Lys Ala Ser Pro Ser AGC CysTGC Phe $\mathbf{T}\mathbf{T}\mathbf{C}$ Trp TGGLeu CIG Thr ACC Pro CCC Leu CTGen

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Ile

Trp

G1Y

Asn

TYr

Phe

Ala

Met

Lys

Phe

Phe

40

 \mathbf{TGG}

 $\frac{1}{2}$

AAT

TAC

TTC

GCC

AAG ATG

TTC

TTC

TAC

 ∞

Д

Figure

Val Ala Cys TGT Val GTGPro CCIIle ATC Ala DDB CCC Leu CICVal GTG50 Ala GCT Leu CIG Phe TTCen 455

Arg CGTLeu Ile ATC LysAAG ATG Met Asn AAC GluGAG Val GIC Asn AAC Arg CGC G1yGGA 9 Arg CGA

Arg CGA ATC Gly 999 TY Γ TAC Leu CIG TYr AAA TAC Lys Ile ATC CAC His Leu CIC Met Leu CIGATG eu

Figure

U Ser TCG Pro CCC Pro CCTPhe TTCHis CAC His CAC Ala GCT G1YCGA GGG Arg Val GTG Glu GAG Val 568

90

Leu CTC Ser \mathbf{TCT} Ser AGC Gln CAG His CAC Asn TCC AAC Ser Val GTC Val 100 GTTVal GTT TYr \mathtt{TAT} Pro CCC ln AG 605

C H Gly Arg CGC 120 CCC Pro CCA CTGLeu GTAGlu Val GAG Met ATG Met ATG G1y9999 Leu Leu 110 Asp

Gly S S S S S Glu Leu Leu Trp Ala GCT CGC GAG CTA CTG TGG Arg LysAAG Ala CCC Ile ATT Pro CCC Val GIG CTD 089

Figure 1D

Ile GTC Val G1yGGA Leu Ala GCA CTG 140 Trp TGG Cys $_{
m LGC}$ Ala CCC Gly Leu CTG CCC Ala CCC er TCT Ñ

Val GIC Ser Ile ATC Ala CCC Gly Asp GAT 999 Thr ACG Arg CGC LysAAG S Arg CGG Asp GAC IleATC he 755

Asp V Ö 170 GAC Gln CAG Thr ACC CICLeu Leu CIG Thr ACC Gln CAG Ala CCC Val GIC Glu GAG Ser $ext{TCT}$ 160 Met

CAC Asn His AAC AGA Arg GAG GGA ACG Thr Gly Glu CCTPro TTTPhe GTG Val TGG Trp AGG GTC Val Arg al 830

Figure 1E

 \mathcal{O} 口 TTCPhe 225 255 Gly Ala TTC AAA CGT Phe Lys Arg 190 CCC Pro ATG CTG Len Met TCC Ser ggc G1yAAT Asn 868

CCC ATA Ile Pro GICVal ATT IleCCC Pro 905 AT CTT GCA GTG CAG GCC CAG GTT Gln Val Gln Ala 200 Leu Ala Val is

Ö 220 AAG Lys AAG $\Gamma \lambda s$ LGC Cys \mathtt{TAC} Tyr TLC Phe GAC Asp CAA Gln TCC TAC TYYSer $\mathbf{I}^{\mathbf{CC}}$ Ser ATG Met GIC Val 943

GTG Val CGG Gln Val Arg TTC ACC TCG GGA CAA TGT CAG GTG Gly Gln Cys Ser Thr Phe CGT CGC Arg Arg AG 1 n980

Figure 1F

K Ü Asp GAT Pro CCA ACA Thr Leu GAA GGG CTG Glu Gly 240 ACG Thr CCC Pro GTGVal Pro CCA CCC Pro CTG Leu 1018

ATG MetCGG CAC TCC Ser His Arg GAC AGA GTC Val Arg Asp GCT Leu Ala CIG 250 CCA GCT Ala Pro GIC Val AC gs 1055

Ö U CGG 270 Gly Arg ATC TCC ACT GAT GGC Asp Thr Ser IleGAA Glu TTC CGG Arg Phe CTC ACT GTT Thr Val 260 Leu 1093

GGT GGG TGA ACCCTGGCTCTGAGCTCTCCTCCCATCTGTCCCCATCTTCCTCCC CACACCTACCCACTGGGCCCTGAAGCAGGGCCAAACCCTTTTCCTT GTCTCCCCTCTCCCCACTTATTCTCCTCTTTGGAATCTTCAACTTCTGAA ly Gly Gly Asp Tyr Leu Lys Lys Pro Gly Gly Gly 280 CTG AAG AAG CCT GGG GGC \mathtt{TAT} 1130 GT GGT GGT GAC 1216 1266 1168

Figure 1G

ACAAGGGGAAGAAGCAGACATCAGGTGCTGCACTCACTTCTGCCCCCTGG GGAGTTGGGGAAAGGAACCCTGGCTGGAGGGGATAGGAGGGCTTTT TCAGTCTCCACATTTCTGGTTTTTCTGTCCCCATAGTACAGTTCTTCAGTG GACATGACCCCACCCCAGCCCTGCAGCCCTGCTGACCATCTCACCAGAC GCCTGCCCTTGCCCAGATGCCCAGGGTCGTGCACTCTCTGGGATACCAGT TGTAGCCTCCTGTCAGTGGGGCTGGACCCTTCTAATTCAGAGGTCTCAT ACAAATCCCCCCCCACTCCAAAGTCCATGGATTCAATGGACTCATTT TGTGAGGAGGACTTCTCGCCCTCTGGCTGGAAGCTGATACCTGAAGCACT AAGGGAGGGAACATTCCATCCCCAGTGGAGTCTCTTCCTATGTGGTCTT TGTCTGTGGGACAGTTGCCTCCCCTCATCTCCAGTGACTCAGCCTACAC CTCTACCCCTCTACCCCCACATTGGCCAGTGGACTCATCCATTTTGGA 1916 1866 1966 1816 1616 1766 1566 1466 1516 1416 1316 1366

Figure 1H

TTTTGCGTGGTTTTTTTTTATTATTATCTGGATAACAGCAAAAAACTG TTTCTTCCTGGTGGCATTAGCCACTCCCTGCCTCTCACTCCAGACCTGTT AATTTATTTCTTTTCTGTTGAGGCTTCCCCCTCTCTGAGCCAGTTTTCA AAAATAAAGAGAGAGAGAAAAAAAA 2216 2016 2116 2166 2066

Figure 2 A

•	4 · 1	•	•	•
50 <u>F</u> <u>F</u> KMA G <u>F</u> VTIRP <u>F</u> SKS	100 -YGIRVEVRG MLGLDVK -FGLKVECRK WAGVKVQLHA	150 -VPI-AKRELVTAKKSL TVTV-GKKSL	SVMSEVAQTL LTQDVRVWV-DTLNKGLENV KKNKRALWV-GTIAEVVNHF KKRRISIWM-KTLKWGLQRL KDFPRPFWLA	250 LAVQAQVPIV LAQQGKIPIV AAIAAGVPII SAVSIMRDFV
40 LWFCSPSAKY C ILVCVFGSIY LIVNAIQAUL	90 RLMLLHIKYL ARCFYHVMKL GHMFGRLAPL WLOLVWYVDW	140 VLPGRC IFPPGCT- IVQ-PP ILAQRSGCLG		240 MLPFKRGAFH MLPFKKGAFH -LPFKTGAFH VLIPRTKGEV
30 LL-LLFLLPT AL-AG RL-IITVIYS PLGLLFLLSG	80 GRNVENMKIL GRQHLAQWIT PRNPKHVATF	130 SSLDLLGMME STLDIFMLGR NNYDMVTASN SDIDWL-IGW	180 IDRKRTGDAI LDRSKRQEAI IDRNNRTKAH LERS-WAKDE	230 T T ASQGLPAPRN
20 VLRSVL-VVL LYIF PLVLVVL	70 VLAIPVCAVR VIASILCTLICLFS EL	120 -PYVVVSNHQ KPYIMIANHQ -NAIYIANHQ EHALIISNHR	170 WLAGVIE WEMALSGTYE WLTGNLL	220 GS SEL RGL AKLLAAQEYA
$\begin{array}{c} 10\\ \underline{\underline{MDLWPGAWM}} -\\ \underline{\underline{MSV}} - \underline{\underline{GRFLY}}\\ \underline{\underline{M}}\\ \underline{\underline{MAI}}\\ \underline{\underline{MAI}} $	60 FYNGWILFLA FYGG FYRRINRFLA	110 AHHF-PPSQ- VVGE-ENLAK PTDA-ESYG- DEETYRSMGK	160 LWAGSAGLAC KYVPFLG LWIPFFGQLY KFLPVIGWSM	210 -FPEGTRNHN -FPEGTRSYT -FPEGTRSRG
ਜਜਜਜ	51 51 51 51	101 101 101 101	151 151 151 151	201 201 201 201 201
Human LPAAT Yeast LPAAT E.coli LPAAT Maize LPAAT	Human LPAAT Yeast LPAAT E.coli LPAAT Maize LPAAT	Human LPAAT Yeast LPAAT E.coli LPAAT Maize LPAAT	Human LPAAT Yeast LPAAT E.coli LPAAT Maize LPAAT	Human LPAAT Yeast LPAAT E.coli LPAAT Maize LPAAT

Figure 2 B

VPTEGLTPDD VPALADR ISTENLTKDK IGEFAEK IDVSQYGKDQ VRELAAH VIHVRMKRHA MSEMPKSDED	340 350 GDYLKKPGGG G* DTTLPPQREAAGK V* PIGRPVKSLL VTLFWSCLLL	390 400 NEPVPSVSIS NDVNTHNEGS GVMHVFIMFS QAERS	440 450
280 GQCQVRVLPP GCMIVRILKP GLVIVEMLPP MLRILKGQSS	330 REISTDGRGG KEIGYSPAIN AELDKEVAE- ATGTFDEEIR	380 HDKKVNKKIK FTAAGMALVT	430
270 YCKKERRETS VSPKYGVENR INLNRLHN IVPKDSPQPT	320 VRHSMLTV-F VRDQMVDT-L CRSIMEQK-I AKDALLDKHL	370 A <u>L</u> Q Q <u>L</u> LSTWRGVA	420 KKMH*
260 PIVMSSYQDF PVVVSNTSTL PVCVSTTSNK PALYDTTV	310 VSKWCKDIFV	360 AIEYA FGAIEFFKWT	410 <u>s</u> <u>v</u> ssaraarnr <u>v</u>
251 251 251 251 251	301 301 301 301	351 351 351 351	401 401 401 401
Human LPAAT Yeast LPAAT E.coli LPAAT Maize LPAAT	Human LPAAT Yeast LPAAT E.coli LPAAT Maize LPAAT	Human LPAAT Yeast LPAAT E.coli LPAAT Maize LPAAT	Human LPAAT Yeast LPAAT E.coli LPAAT Maize LPAAT

Figure 3A

10 20 30 40 50 60									•
20 30 40 GGCGGCGCC TCGGGCGCC GGCCGGGCCA 140 150 160 TGCTGTTGCT GCTGCTGCTG GTGCAGCTGA 140 210 210 220 CCCTGTACTG CGCGCTGTGC TTCACGGTGT 260 270 280 AGTACTTTTA CGGGCTCCGC TTCGAGGTGC CCTGTGTCAT CGTCTCCAAC CACCAGAGCA CCTGTGTCAT CGTCTCCAAC CACCAGAGCA TTCCGGAGCG CTGCGTGCAG ATCGCCAAGC TTCCGGAGCG CTGCGTGCAG GTCTTCTTCA 1500 440 450 TTCATCATGTA CCTCGGGGGC GTCTTCTTCAA CAGTGATGC CGACCTGGGC GAGCGCATGG CAGTGATGC CGACCTGGGC GAGCGCATGG	60 GCCGTGTCTG	120 CGAGTTCTAC	180 CTCGCTCGTC	240 CTGGTTCGTG	300 CAGGCTGCAĠ	360 GATGGGCCTC	CTTCCTG	GCGCTCI	CCTCAAA
20			170 CCGCCGTGGC	230 GCATCATCGG			410 GGGAGCTGCT		530 TCAGGGAGAA
20 GGCGGCGCCG 7 80 TGCTGTTGCT C 200 CCCTGTACTG C 320 CCTGTGTCTTTA (380 TTCCGGAGCG TTCCGGAGCG TTCCGGAGCG TTCCGGAGCG TTCCGGAGCG	40 GGCCGGGCCA	100 GTGCAGCTGA	160 TTCACGGTGT	220 GAGAACATGA	280 TTCGAGGTGC		400 ATCGCCAAGC	. 460 GTCTTCTTCA	
	30 rceecccce	90 GCTGCTGCTG	150 cececrerec	210 CCGGACGGTG	•	330 CGTCTCCAAC	390 CTGCGTGCAG	450 CCTCGGGGGC	
10 GGAGGGGGG GCCGGGGGCG 130 GCCAAGGTCG TGCCTGCTGT 310 GAGGCCCGTC ATGGAGGTCC 430 ACTGCCATGA		80 TGCTGTTGCT	140 CCCTGTACTG	200 GCCACGGCGG	260 AGTACTTTTA	320 CCTGTGTCAT	380 TTCCGGAGCG	440 TCATCATGTA	500 CAGTGATGGC
	10 GGAGCGAGCT	70	130 GCCAAGGTCG	190 TGCCTGCTGT	250 CGAAGCTTCA	310 GAGGCCCGTC	370 ATGGAGGTCC	430 CCCGTGGGCC	490 ACTGCCATGA

Figure 3B

550	560	570	580	590	600	
TGGATCTATC C	CCGAGGGTAC	TCGCAACGAC	AATGGGGACC	TGCTGCCTTT	TAAGAAGGGC	
610	620	630	640	650	660	
GCCTTCTACC T	TGGCAGTCCA	GGCACAGGTG	CCCATCGTCC	CCGTGGTGTA	CTCTTCCTTC	
670	680	690	700	710	720	
TCTCCTTCT	ACAACACCAA	GAAGAAGTTC	TTCACTTCAG	GAACAGTCAC	AGTGCAGGTG	
730 CTGGAAGCCA	740 TCCCCACCAG	750 CGCCTCACT	750 770 GCGGCGGACG TCCCTGCGCT	770 TCCCTGCGCT	780 CGTGGACACC	
790	800	810	820	830	820 830 840	
TGCCACCGGG	CCATGAGGAC	CACCTTCCTC	CACATCTCCA	AGACCCCCCA	CACATCTCCA AGACCCCCCA GGAGAACGGG	
850	860	870	880	890	900	
GCCACTGCGG	GGTCTGGCGT	GCAGCCGGCC	CAGTAGCCCA	GACCACGGCA	GGGCATGACC	
910	920	930	940	950	960	
TGGGGAGGGC	AGGTGGAAGC	CGATGGCTGG	AGGATGGGCA	GAGGGGACTC	CTCCCGGCTT	
970	980	990	1000	1010	1020	•
CCAAATACCA	CTCTGTCCGG	CTCCCCCAGC	TCTCACTCAG	CCCGGGAAGC	AGGAAGCCCC	
1030 TTCTGTCACT	G	1040 1050 GTCTCAGAC ACAGGCCCCT	1060 GGTGTCCCCT	1070 GCAGGGGGCT	1080 CAGCTGGACC	

Figure 3C

1320 GTCAGCACTG 1380 AAAAAAAAA 1440	1310 AATCTGTGGG GTCAGCACTG 1370 1380 AAAAAAAA 1430 1440	1300 TGGCCTGAAG 1360 TCTTGGAAAA	TGG	1280 1290 1300 1310 TCGGGGCCTG CTGCTCCTGC TGGCCTGAAG AATCTGTGGG 1340 1350 1360 1370 CTGTTTTTTT ATAAACACA TCTTGGAAAA AAAAAAAAA 1400 1410 1420 1430
1380 AAAAAAAAA	1370 AAAAAAAAA	1360 TGGAAAA	TCT	1350 ATAAACACAC
GTCAGO	1310 AATCTGTGGG	1300 sccrgaag	ŢĞ	1290 CTGCTCCTGC TG
1260 GGGCCACAGG	1250 CACGCACCCT	1240 CCCAGACT	ĞŢ	1220 1230 1240 GGAGGACCCC GAGGCCAGGA GTCCCAGACT
1200 CGATGGCCCA	1190 ACAAGGCCCC	1180 scrgagcc	999	1170 1180 1190 1200 GCCCGCTGGT GGGCTGAGCC ACAAGGCCCC CGATGGCCCA
1140 GGGNTGATAA	1120 1130 CCACGGCACC TCTGGGNGCT	1120 CGGCACC		1110 GGACTCGCGC CCA

Figure 4 A

CCG	CTG Leu 20	GCG Ala
50 TGG Trp	CAG	140 TGC Cys
CTG Leu	GTG Val	140 TAC TGC TYr CYS
GAG Glu	90 CTG Leu	CTG
10 ATG Met	CTG	130 GTC GCC GVal Ala I
ညည်း	CTG	1; GTC Val 30
ງຄວວຄ	80 CTG Leu	AAG Lys
30 20GG	TTG	GCC
ວອນອະ	CTG	120 TAC TYr
TCGC	70 CTG Leu	TTC
20205	3CG Ala 10	GAG Glu
ວອອວເ	GCC GCG (Ala Ala	110 GCG GCC (Ala Ala (
10 CTGC	GCC	GCG Ala
CGAG	60 CTG Leu	CGC
10 20 30 40 GGAGCGAGCTGGCGCCCGGCCCGGGCC ATG 0	60 TGT CTG Cys Leu	100 AGC Ser

CTG Leu 50	TGG
CTG	230 3 GGC 6 G1y
TGC	ATC Ile
180 GTC Val	ATC Ile
CTC	220 ATG AGC Met.Ser 60
TCG Ser	22 ATG Met 60
70 GCC Ala	AAC Asn
170 GTG GCC Val`Ala	GAG Glu
GCC Ala	210 GTG Val
TCC Ser	ACG Thr
160 GTG TCC Val Ser 40	CGG
ACG Thr	900 GGC Gly
TTC	2 GGC G1Y
150 TGC Cys	200 C CAC GGC GGC His Gly Gly
CTG	90 TGC Cys

TTC Phe Phe CGG CGG CGG Ser Ser CTT CTT CTG Leu Leu Leu ATC Ile		CGA Arg CCCG Pro CAC His GAG GAG Arg Arg	AGC Ser 290 CGC Arg Gln GTG Val Val CAG	### 25 TTC	Lys Lys Lys Lys Leu CTG Val Val CTC Leu Ser	TAC TYT TYT 300 CAG Gln Gln Gln Gln ATC TAC ATC TYT ATC SAG	TTT Phe Phe GAG GAC ASP ASP ATC Ile ATC Ile ATC Thr	60 TAC TYT GCC Ala GCC Ala 140 TAC TYT TYT	GGG GLY GGT Arg Arg Arg Arg Lys Lys Lys Lys Lys Arg Arg	CTC Leu O CCC CCC Gly Arg Arg GGG Gly	270 CGC Arg Cys Cys CTC Leu Glu G10 G10 G10	Figure 4B	GTG CGA AGC TTC AAG TAC TTT TAC GGG CTC Val Arg Ser Phe Lys Tyr Phe Tyr Gly Leu	GAC CCG CGC AGG CTG CAG GAG ASP Pro Arg Arg Leu Gln Glu	330 340 350 AAC CAC CAG AGC ATC CTG GAC ATG ATG GGC ASN His Gln Ser Ile Leu Asp Met Met Gly 100	380 390 4CCCG GAG CGC CAG ATC GCC AAG Pro Glu Arg Cys Val Gln Ile Ala Lys 120	420 GGG CCC GTG GGC CTC ATC ATG TAC CTC GGG GGC GTC GIY Pro Val Gly Leu Ile Met Tyr Leu Gly Gly Val	AAC CGG CAG CGC TCT AGC ACT GCC ATG ACA GTG ATG ASS ASS ASS ASS ASS ASS ASS ASS ASS AS
### Figure 4 B 250 250 250 250 250 250 250 250 250 25	Figure 4 B 250 260 CGA AGC TTC AAG TAC TTT TAC GGG CTC Arg Ser Phe Lys Tyr Phe Tyr Gly Leu 290 300 310 CCG CGC AGG CTG CAG GAG GCC CGT CCC CGT CCT Pro Arg Leu Gln Glu Ala Arg Pro 90 350 CAC AGC ATC CTG GAC ATG ATG Pro 90 350 GAG CGC CTG CAG GAC ATG ATG ATG CGC GGG GAG CGC CGT CAG CGG GAG CGC CAG CGG GAG CGC CAG CGG GAG CGC TCT AGG CAG CGG TAC ATG TAC	Figure 4 B 250 250 FTC AAG TAC TTT TAC GGG CTC Phe Lys Tyr Phe Tyr Gly Leu 300 310 AGG CTG CAG GAG GCC CGT CCC ATG CAG CAC CAT CTG CAG ATG CGC CGT CGC CAG CAG CGC CGT CGC ATG ATG ATG ATG ATG CGC CAG CGG CAG CGG CAG CGG CAG CGG CAG CGG CAG CGG CAG CA	Figure 4 B 250 250 FTC AAG TAC TTT TAC GGG CTC Phe Lys Tyr Phe Tyr Gly Leu 300 310 AGG CTG CAG GAG GCC CGT CCC ATG CAG CAC CAT CTG CAG ATG CGC CGT CGC CAG CAG CGC CGT CGC ATG ATG ATG ATG ATG CGC CAG CGG CAG CGG CAG CGG CAG CGG CAG CGG CAG CGG CAG CA	260 TTT TAC GGG CTC She Tyr Gly Leu 310 330 GAC GGT CCC GAC ATG ATG GGC ASP Met Met Gly ATC GCC AAG CGG Ile Ala Lys Arg 120 440 ATG TAC CTC GGG Met Tyr Leu Gly Thr Ala Met Thr Thr Ala Met Thr	260 TTT TAC GGG CTC She Tyr Gly Leu 310 330 GAC GGT CCC GAC ATG ATG GGC ASP Met Met Gly ATC GCC AAG CGG Ile Ala Lys Arg 120 440 ATG TAC CTC GGG Met Tyr Leu Gly Thr Ala Met Thr Thr Ala Met Thr	260 TTT TAC GGG CTC She Tyr Gly Leu 310 330 GAC GGT CCC GAC ATG ATG GGC ASP Met Met Gly ATC GCC AAG CGG Ile Ala Lys Arg 120 440 ATG TAC CTC GGG Met Tyr Leu Gly Thr Ala Met Thr Thr Ala Met Thr	GGG CTC Gly Leu 310 CGT CCC Arg Pro 90 Arg GGC Met Gly AAG CGG Lys Arg 120 AAG CGG Leu Gly AGG ACA	GGG CTC Gly Leu 310 CGT CCC Arg Pro 90 Arg GGC Met Gly AAG CGG Lys Arg 120 AAG CGG Leu Gly AGG ACA	270 CTC CGC Leu Arg CCC TGT Pro Cys 360 GGC CTC Gly Leu Arg Glu Arg Glu GGG GGC GIY GIY	270 CGC Arg Cys Cys CTC Leu Glu G10 G10 G10			ŤTC Phe	3 GTC Val	ATG	CTG Leu	GTC Val	ATG
### Figure 4 B 250 250 250 250 250 250 250 250 250 25	Figure 4 B 250 260 CGA AGC TTC AAG TAC TTT TAC GGG CTC Arg Ser Phe Lys Tyr Phe Tyr Gly Leu 290 300 310 CCG CGC AGG CTG CAG GAG GCC CGT CCC CGT CCT Pro Arg Leu Gln Glu Ala Arg Pro 90 350 CAC AGC ATC CTG GAC ATG ATG Pro 90 350 GAG CGC CTG CAG GAC ATG ATG ATG CGC GGG GAG CGC CGT CAG CGG GAG CGC CAG CGG GAG CGC CAG CGG GAG CGC TCT AGG CAG CGG TAC ATG TAC	Figure 4 B 250 250 FTC AAG TAC TTT TAC GGG CTC Phe Lys Tyr Phe Tyr Gly Leu 300 310 AGG CTG CAG GAG GCC CGT CCC ATG CAG CAC CAT CTG CAG ATG CGC CGT CGC CAG CAG CGC CGT CGC ATG ATG ATG ATG ATG CGC CAG CGG CAG CGG CAG CGG CAG CGG CAG CGG CAG CGG CAG CA	Figure 4 B 250 250 FTC AAG TAC TTT TAC GGG CTC Phe Lys Tyr Phe Tyr Gly Leu 300 310 AGG CTG CAG GAG GCC CGT CCC ATG CAG CAC CAT CTG CAG ATG CGC CGT CGC CAG CAG CGC CGT CGC ATG ATG ATG ATG ATG CGC CAG CGG CAG CGG CAG CGG CAG CGG CAG CGG CAG CGG CAG CA	260 TTT TAC GGG CTC She Tyr Gly Leu 310 330 GAC GGT CCC GAC ATG ATG GGC ASP Met Met Gly ATC GCC AAG CGG Ile Ala Lys Arg 120 440 ATG TAC CTC GGG Met Tyr Leu Gly Thr Ala Met Thr Thr Ala Met Thr	260 TTT TAC GGG CTC She Tyr Gly Leu 310 330 GAC GGT CCC GAC ATG ATG GGC ASP Met Met Gly ATC GCC AAG CGG Ile Ala Lys Arg 120 440 ATG TAC CTC GGG Met Tyr Leu Gly Thr Ala Met Thr Thr Ala Met Thr	260 TTT TAC GGG CTC She Tyr Gly Leu 310 330 GAC GGT CCC GAC ATG ATG GGC ASP Met Met Gly ATC GCC AAG CGG Ile Ala Lys Arg 120 440 ATG TAC CTC GGG Met Tyr Leu Gly Thr Ala Met Thr Thr Ala Met Thr	GGG CTC Gly Leu 310 CGT CCC Arg Pro 90 Arg GGC Met Gly AAG CGG Lys Arg 120 AAG CGG Leu Gly AGG ACA	GGG CTC Gly Leu 310 CGT CCC Arg Pro 90 Arg GGC Met Gly AAG CGG Lys Arg 120 AAG CGG Leu Gly AGG ACA	270 CTC CGC TTC Leu Arg Phe CCC TGT GTC Pro Cys Val 360 GGC CTC ATG Gly Leu Met Arg Glu Leu Arg Glu Leu 450 GGG GGC GTC Gly Gly Val Gly Gly Val Thr Val Met	270 CGC TTC Arg Phe Cys Val 360 CTC ATG CTC ATG Glu Leu 450 GGC GTC GIY Val GTG ATG	TTC Phe GTC Val Leu GTC Val Met		GAG Glu	320 ATC Ile	GAG Glu	110 CTC Leu	TTC	500 GCC Ala
### Figure 4 B 250 250 250 250 250 250 250 250 250 25	Figure 4 B 260 270 250 270 250 270 250 270 250 270 260 270	## 15gure 4 B 250 270 FTC AAG TAC TTT TAC GGG CTC CGC TTC GAG Phe Lys Tyr Phe Tyr Gly Leu Arg Phe Glu 70 300 310 320 AGG CTG CAG GAG GCC CGT CCC TGT ATC ATC ATG Phe Glu Ala Arg Pro Cys Val Ile Agg Arg GGC CTC ATG GAG Ser Ile Leu Asp Met Met Gly Leu Met Glu Leu Asp Met Met Gly Leu Met Glu Leu Cys Val Ile Agg ATG GGG GAG CTC CTC GGG GAG CTC TTC GLy Leu Ile Ala Lys Arg Glu Leu Leu CLys Leu Ile Agg TAC CTC GGG GGC GTC TTC GLy Leu Ile Agg TAC CTC GGG GGC GTC TTC GLy Leu Ile Agg TAC CTC GGG GGC GTC TTC GLy Leu Ile Agg TAC CTC GGG GGC GTC TTC GLy Leu Ile Agg TAC ATG ACA GTG ATG ATG GCC CTC AGG GCC CTC AGG GGC GTC TTC GGG GGC CTC AGG GGC GTC TTC GGG GGC GTC TTC T	## 15gure 4 B 250 270 FTC AAG TAC TTT TAC GGG CTC CGC TTC GAG Phe Lys Tyr Phe Tyr Gly Leu Arg Phe Glu 70 300 310 320 AGG CTG CAG GAG GCC CGT CCC TGT ATC ATC ATG Phe Glu Ala Arg Pro Cys Val Ile Agg Arg GGC CTC ATG GAG Ser Ile Leu Asp Met Met Gly Leu Met Glu Leu Asp Met Met Gly Leu Met Glu Leu Cys Val Ile Agg ATG GGG GAG CTC CTC GGG GAG CTC TTC GLy Leu Ile Ala Lys Arg Glu Leu Leu CLys Leu Ile Agg TAC CTC GGG GGC GTC TTC GLy Leu Ile Agg TAC CTC GGG GGC GTC TTC GLy Leu Ile Agg TAC CTC GGG GGC GTC TTC GLy Leu Ile Agg TAC CTC GGG GGC GTC TTC GLy Leu Ile Agg TAC ATG ACA GTG ATG ATG GCC CTC AGG GCC CTC AGG GGC GTC TTC GGG GGC CTC AGG GGC GTC TTC GGG GGC GTC TTC T	260 TTT TAC GGG CTC CGC TTC GAG She Tyr Gly Leu Arg Phe Glu 310 320 330 340 ATC GCC CGT CCC TGT GTC ATC 350 ATC ATG GGC CTC ATG GAG ASP Met Met Gly Leu Met Glu A10 ATC GCC AAG CGG GAG CTG CTC Ile Ala Lys Arg Glu Leu Leu 120 ATG TAC CTC GGG GGC GTC TTC ATG TAC CTC GGG GGC GTC TTC ATG TAC TTC ATG GGC ATG TAC TTC ATG GAG ATG TAC TTC ATG ATG GCC TTC ATG ATG ATG ATG ATG Thr Ala Met Thr Val Met Ala	260 TTT TAC GGG CTC CGC TTC GAG She Tyr Gly Leu Arg Phe Glu 310 320 330 340 ATC GCC CGT CCC TGT GTC ATC 350 ATC ATG GGC CTC ATG GAG ASP Met Met Gly Leu Met Glu A10 ATC GCC AAG CGG GAG CTG CTC Ile Ala Lys Arg Glu Leu Leu 120 ATG TAC CTC GGG GGC GTC TTC ATG TAC CTC GGG GGC GTC TTC ATG TAC TTC ATG GGC ATG TAC TTC ATG GAG ATG TAC TTC ATG ATG GCC TTC ATG ATG ATG ATG ATG Thr Ala Met Thr Val Met Ala	260 TTT TAC GGG CTC CGC TTC GAG She Tyr Gly Leu Arg Phe Glu 310 320 330 340 ATC GCC CGT CCC TGT GTC ATC 350 ATC ATG GGC CTC ATG GAG ASP Met Met Gly Leu Met Glu A10 ATC GCC AAG CGG GAG CTG CTC Ile Ala Lys Arg Glu Leu Leu 120 ATG TAC CTC GGG GGC GTC TTC ATG TAC CTC GGG GGC GTC TTC ATG TAC TTC ATG GGC ATG TAC TTC ATG GAG ATG TAC TTC ATG ATG GCC TTC ATG ATG ATG ATG ATG Thr Ala Met Thr Val Met Ala	270 GGG CTC CGC TTC GAG Gly Leu Arg Phe Glu 310 GGT CCC TGT GTC ATC Arg Pro Cys Val Ile 90 ATG GGC CTC ATG GAG Met Gly Leu Met Glu Lys Arg Glu Leu Leu 120 450 CTC GGG GGC GTC TTC Leu Gly Gly Val Phe Leu Gly Gly Val Phe 490 ATG ACA GTG ATG GCC Met Thr Val Met Ala	270 GGG CTC CGC TTC GAG Gly Leu Arg Phe Glu 310 GGT CCC TGT GTC ATC Arg Pro Cys Val Ile 90 ATG GGC CTC ATG GAG Met Gly Leu Met Glu Lys Arg Glu Leu Leu 120 450 CTC GGG GGC GTC TTC Leu Gly Gly Val Phe Leu Gly Gly Val Phe 490 ATG ACA GTG ATG GCC Met Thr Val Met Ala	270 CGC TTC GAG Arg Phe Glu 320 TGT GTC ATC Cys Val Ile Leu Met Glu GAG CTG CTC Glu Leu Leu 450 GGC GTC TTC Gly Val Phe GIY Val Phe GTG ATG GCC Val Met Ala	270 Arg Phe Glu 320 TGT GTC ATC Cys Val Ile Leu Met Glu GAG CTG CTC Glu Leu Leu 450 GGC GTC TTC GIY Val Phe GIY Val Phe 500 GTG ATG GCC Val Met Ala	TTC GAG Phe Glu 320 GTC ATC Val Ile ATG GAG Met Glu Leu Leu Leu Leu Leu Leu S10 ATG GCC Met Ala		Ŭ >	GTC Val	GTC Val 110	TTC		

Figure 4C

			•		
TAT	Tyr 170	AAG	GTC Val 200	AAG Lys	GCC Ala 230
	Ile Ile	590 TTT Phe	ATC Ile	680 ACC AAG Thr Lys	GAA G1u
	Trp	590 CCT TTT Pro Phe	CCC	ACC Thr	CTG Leu
	Val	CTG	630 GTG Val	AAC Asn	720 GTG Val
AAA	Lys	to CTG Leu	cAG Gln	670 TTC TAC Phe Tyr 210	Gre CAG (Val Gln
ن تار	ren	580 GAC CTG Asp Leu 180	GCA Ala	67 TTC Phe 210	GTG
530	Glu Asn	666 61y	620 GTC CAG Val Gln	TCC	10 ACA Thr
2 2	Glu	AAT Asn	GTC Val	TCC	7 GTC Val
ָרָ כ	Arg	570 GAC ASP	GCA (660 TTC Phe	ACA
0 0	Met Val	AAC Asn	o CTG Leu	TCC	700 TCA GGA Ser Gly 220
52 2mr	Met 160	CGC	61 TAC TYT 190	TCT	700 TCA G Ser G 220
ָרָ ע	Arg	560 ACT Thr	TTC	650 GTG TAC Val TYr	ACT
ر د	Glu Glu	560 GGT ACT Gly Thr	GCC		TTC
510	G17	GAG Glu	600 GGC G1Y	GTG Val	690 TTC Phe
	ren	550 CCC Pro	AAG Lys	640 CCC Pro	AAG '
					• •

		POLYPEPTIDE (As A Inventors: David W. LE Atty. Docket No.: 077
GTG Val	TCC Ser 260	CAG Gln
770 3 CTC a Leu	ATC Ile	860 GTG Val
7 GCG Ala	CAC	8 GGC Gly
CCT	810 CTC Leu	TCT

TTC

800 AGG ACC

ACC

Met

CGG GCC AAR ARG ARG A

CAC

780 ACC

TGC

GAC

GAC GTC 760

GCG GCG

Gly Leu Thr

Pro Thr Ser

GGC CTC

740 CCC ACC AGC (

ATC

Figure 4D

Asp Val 240

850 S ACT GCG GGG TCT GGC GTG CAG A Thr Ala Gly Ser Gly Val Gln 270	870 880 890 900 910 920 CCG GCC CAG CCCAGACCAGGCAGGCATGACCTGGGGAGGGCAGGGAAGC
860 GTG Val	GTG
8 660 61y	910 GGGCAG
TCT Ser	SGAGC
850 G GGG a Gly	o CTGG(
8: GCG Ala 270	900 TGACC
ACT	GGCA
GCC Ala	890 GCAG
840 GGG G1y	CACG
AAC	0 AGAC
GAG Glu	880 CCCA(
830 CAG Gln	TAG
CCC	870 GCC CAG TAG
840 G ACC CCC CAG GAG AAC GGG GCC AC s Thr Pro Gln Glu Asn Gly Ala Th	870 GCC
820 AAG Lys	ອວວ

	CTCTGTCCGG
	940 950 960 970 980
	970 STCCTCCGGC
	960 CAGAGGGGA
Gln ***	950 GGAGGATGGG
Pro Ala	940
	. 0

CTCAGAC 1100 AGGGCAG
1000 1010 1020 1030 1040 CTCCCCCAGCTCTCACTCAGCCCGGAAGCAGGAAGCCCCTTCTGTCACTGGTCTCAGAC TCCCCCCAGCTCTCACTCAGCCCGGAAGCAGCAGGAAGCCCCTTCTGTCACTGGTCTCAGAACTCAGCTGGAAGCCCCTCCCCGGGGCTCCAGGGGGGCTCAGCTGGACCCTCCCCGGGGCTCGAGGGGGCCAG
1040 AGCCCCTTCT 1080 TGGACCCTCC
1030 GAAGCAGGA 1070 GGGCTCAGC
1020 CTCAGCCCGG 1060 CCCCTGCAGG
1010 CCAGCTCTCAC 1050 CCCTGGTGTC
1000 CTCCCCC

Figure 4 E

1110	1120 GGACTCGC	1130 GCCCACGGCAC	1140 CTCTGGGNGC	1150 CTGGGNTGATA	1120 1130 1140 1150 1160 GGACTCGCGCCCACGGCACCTCGGGNGCTGGGNTGATAAAGATGAGGCTTGCGGCTGTG	
1170	1180 GCCCGCTG	1190 GTGGGCTGAGC	1200 CACAAGGCCC	1210 CCCGATGGCCC	1180 1190 1200 1210 1220 GCCCGCTGGTGGCCTGAGGCCCCCGATGGCCCAGGAGGATGGGAGGACCCC	
1230	1240 GAGGCCAG	1250 GAGTCCCAGAC	1260 TCACGCACC	1270 CTGGGCCACAG	1240 1250 1260 1270 1280 GAGGCCAGGAGTCCCAGACTCACGCACCTGGGCCACAGGGAGCCGGGAATCGGGGCCTG	
1290	1300 CTGCTCCT	1310 GCTGGCCTGAA	1320 AGAATCTGTG	. 1330 sggtcagcact	1300 1310 1320 1330 1340 CTGCTCCTGCTGAAAATCTGTGGGGTCAGCACTGTACTCCGTTGCTGTTTTTT	•
1350	1360	1360 1370 1380 1380 1370 1380	1380	AAAAAAAAA	AAAA	

Figure 5 A

Alignment of LPAAT Sequences.

10 20 40 50 1	1 MAKIRUSS-L RNRRQLKP AVAATADD DKDGVFMV 1 MDASCASSFL RGRCLESCFK ASFGMSQPKD AAGQPSRRPA DADDFFTVDD	51 QLSRAE FYAKVAL-YC ALGTVSAVA SLVCLLGGG RIVENM-SII 51 TWFCS BAK YFFKMAF-YN GWILFIAVLA IPVCAV-RG RNVENM-KIL	51 GCG FYG <u>VIA SILCTLIGKO HLAQWI-TAR</u> 51 G		35171	51 DRWITVILSV VRIARCEL- SMVITIVM MIMILILEWP YAKIKUSINA
Human LPAAT-β Human LPAAT-α Yeast LPAAT E.coli LPAAT H.influenzae	S.typhimuriu L.douglassi C. nucifera	Human L.PAAT-β Himan I.PAAT-α	Yeast LPAAT	H.influenzae	L.douglassi	C. nucifera

Figure 5 B

150 ILDMYGIMEN SILDILGWME TIDIEMIGRI N NYDWYTAS N NYDWY	K AHS—TI	
110 120 130 140 150 101 GWFWSF KYFYGLRFEY ROPRRIQEAR PCYTVSNHOS ILLIMYGIMEY 101 RLMIHI KYLYGIRVEY RGAHFPPSQ PYVVSNHOS SIDILGWMEY 101 GTWFGRLFY YPLFGLKVEC RYPTDAESYG NALYTANHON NYDMYTASNI 101 ARWFGRLFY YPLFGLKVEC RYPTDAESYG NALYTANHON NYDMYTASNI 101 ARWFGRLFY YPLFGLKVEC RYPTDAESYG NALYTANHON NYDMYTASNI 101 GHMFGRLFY YPLFGLKVEC RYPTDAESYG NALYTANHON NYDMYTASNI 102 GHMFGRLFY YPLFGLKVEC RYPTDAESYG NALYTANHON NYDMYTASNI 103 GHMFGRLFY YPLFGLKVEC RYPTDAESYG NALYTANHON NYDMYTASNI 104 GHMFGRLFY YPLFGLKVEC RYPTDAESYG NALYTANHON NYDMYTASNI 105 ARWFGRLFY YPLFGLKVER FY GLYMLGGY FFINRORSYG ANTVMAIL 110 GHMFGRLFY YPLFGLKVEF TGILYMVTGY IFIDRINRIK AHYTIAEV 111 REGCYNTAK KSLIMIPFF TGILYMVTGY IFIDRINRIK AHYTIAEV 112 VQPPTVTVGK KSLIMIPFF TGILYMVTGY IFIDRINRIK AHYTIAEV 113 VQPPTVTVGK KSLIMIPFF TGILYMVTGY IFIDRINRIK AHYTIAEV	KSLIMIPFF TGOLYWLTCN ILIDRINNRAK AHS—TIAAV KEVIWYPILG Q—LYTIAH IRIDRSNPAA AICSFIMKEA	
130 RDPRRLQEAR VGEENLAK-K VGEENLAK-K C RKPTDAESY H RIPODOXOI SC RKPADAEN OGSEHIKKRA 180 GLIMYLGG GLACWLAG	G Q LYTLAH	G VE1 412 VALES
120FYGLRFEVINGIRVENMLGLDVKVMLGLDVKVMLGLDVKVMLGLDVKVMLGLDVKVMLGLDVKVMLGLDVKV	K KSLIWIPFE K KEVIWYPIL	K KE LLWYFLF
GWEVRSF KY - RLMITHI KY - CEY-HVMKL - GHMEGRL -FT GHNFGRL -FT GHIGGLV - GHUTGRV - 160 LP ERCV PLAR VOP PTVT GG VOP	VOPPIVIVG APIGIVGVA	
101 101 101 101 101 101 101 101 101 101	1212	<u>ነ</u>
Human LPAAT-6 Yeast LPAAT E.coli LPAAT H.influenzae S.typhimuriu L.douglassi C. nucifera Human LPAAT-6 Human LPAAT-7 Human LPAAT-7 Human LPAAT-4	S. typhimuriu L. douglassi	وسرما بمرسد م

Figure 5C

,	·
MI YPEGTRN DNGDL—LPF KKGAFHL—A VQAQVPIVPV WVFPEGTRS YISELIMLPF KKGAFHL—A QQGGI PIVPV WWFPEGTRS YISELIMLPF KKGAFHL—A QQGGI PIVPV WWFPEGTRS YISELIMLPF KTGAFHL—A QQGGI PIVPV WWFPEGTRS YISELIMLPF KTGAFHL—A QQGGI PIVPV IWMFPEGTRS RGRGL—LPF KTGAFHFHAA ISAGVPI IPV LIMFPEGTRS GOGRL—LPF KKGFVHL—A LQSHLPIVPM LITFPEGTRS GOGRL—LPF KKGFVHL—A LQSHLPIVPM LITFPEGTRS KTGRL—LPF KKGFVHL—A LQSHLPIVPM	260 270 280 300 300 251 VYSS FSSE YNTKKF FTS GTVTVQVLEA IPTSGLTAD VPALVDTCHR GCOVRVLPP VPT EGLT PLD VPALADRYRH IST VVSNTSTL VSPKYGV FNR GCOVRVLPP ISTENLITKDK ICEFAEKVRD INTINRIHN GLVTVEMLPP IDVSGYGKDQ VRELAAHCR-151 VCSSTH NK INTINRIHN GLVTVEMLPP IDVSGYGKDQ VRELAAHCR-151 VCSSTH NK INTINRINN GLVTVEMLPP IDVSGYTKDN VRDLAAYCHE INTODWTVIK IDDXVKMIHD INTODWTVIK IDDXVKMIHD INTODWTVIK IDDXVKMIHD
WILYPEGTRN DNGDL—LPF KKGAFYL—A VQAQVPIVPV WWVFPEGTRN HNGSM—LPF KRGAFHL—A VQAQVPIVPU IMMEPEGTRS YISELIMLPF KKGAFHL—A QQGYLPIVPV IWMEPEGTRS RGRGL—LPF KTGAF—HAA LAAGVPLIPV IWMEPEGTRS RGRGL—LPF KTGAF—HAA LAAGVPLIPV IWMEPEGTRS RGRGL—LPF KTGAF—TFHAA LAAGVPLIPV IMMEPEGTRS GOGRL—LPF KTGAF—TFHAA LAAGVPLIPV LIMEPEGTRS GOGRL—LPF KKGFVHL—A LQSHLPIVPM LITEPEGTRS KTGRL—LPF KKGFVHL—A LQSHLPIVPM	YCKKERETS GIVTVQNLEA IPTSGLEAD VPALVDTCH YCKKERRETS GQQVRVLPP VPTEGLEDD VPALADEVRH VSPKKJVENR GMIVRILKP ISTENLITKOK IGEFAEKVRD NK INLARIHN GLVTVEMLPP IDVSQKGKDQ VRELAAHCRE NK INLARINN GKVICEIMDP IDVSGYTKDN VRDLAAYCHE NKVNLARINN GLVTVEMLPP VDVSGKGKDQ VRELAAHCRE TRKGIFRVRP VPITVKYLPP INTDDWTVDK IDDXVKMIHI TRKGIFRVRP VPITVKYLPP INTDDWTFEK INHYVEMIHE
CERMARENLA VMI YPEGTRN DNGDL—LPF KR 1 AQTLITQDVR VWVFPEGTRN HNGSM—LPF KR 1 LENVKKNKRA LWVFPEGTRS YTSELIMLPF KK 1 LENVKKRRIS IWMFPEGTRS RGRGL—LPF KT 1 ARRINEDNIS IWMFPEGTRS RGRGL—LPF KT 1 VNHFKKRRIS IWMFPEGTRS RGRGL—LPF KT 1 VNHFKKRRIS IWMFPEGTRS GOGRL—LPF KT 1 VRVITEKNIS LIMFPEGTRS GOGRL—LPF KT 1 VRVITEKNIS LIMFPEGTRS GOGRL—LPF KT 1 VRVITEKNIS LIMFPEGTRS GOGRL—LPF KT 2 LIMFPEGTRS KTGRL—LPF KT 2 LIMFPEGTRS KTGRL—LPF KT 3 LIMFPEGTRS KTGRL—LPF KT 3 LIMFPEGTRS KTGRL—LPF KT 4 LIMFPEGTRS KTGRL—LPF KT 5 LIMFPEGTRS KT 5	GIVIVOLEA GOOVRULEA GOOVRULER GOMIVELKE GEVIVEMEP GEVIVEMEP GEVIVEMEP GEVIVEMEP GEVIVEMEP
VWI YPEGTRN VWVFPEGTRN LWVFPEGTRS IWMFPEGTRS IWMFPEGTRS IWMFPEGTRS LIMFPEGTRS LIMFPEGTRS LIMFPEGTRS	YNTKKKFETS YCKKERRETS VSPKYGVENR NKINIARIHN NKINIARWDN NKINIARWDN NKYNIARIHN NKYNIARIHN NKYNIARIHN NKYNIARIHN NKYNIARIHN
GERMARENLA AQTLITQDAR LENVEKNERA VNHFERRES ARRI NEDNIS VNHFERRES VNHFERRES VNHFERRES VRVITEKNIS VRVITEKNIS ARAWENIS	VYSSFSS-F VMSSYQD-F VVSNTST-L CVSTTS VCSSTH ILTGTHLAW VLTGTHLAW
201 201 201 201 201 201 201 201	251 251 251 251 251 251 251 251
Human LPAAT-β Human LPAAT-α Yeast LPAAT E.coli LPAAT H.influenzae S.typhimuriu L.douglassi C. nucifera	Human LPAAT-β Human LPAAT-α Yeast LPAAT E.coli LPAAT H.influenzae S.typhimuriu L.douglassi C. nucifera

Replacement Sheet
Appl. No.: 10/667,494

Title: HUMAN LYSOPHOSPHATIDIC ACID
ACYLTRANSFERASE GAMMA-1
POLYPEPTIDE (As Amended)
Inventors: David W. LEUNG et al.
Atty. Docket No.: 077319-0381

Figure 5D

350	KNEPVPSVSI					•	•	•			•	•	•
340	GSGVQPAQ* KKPGGGG* PPQAIEYAAL QHDKKVNKKI KNEPVPSVSI				390					•		•	
330		R EAAGKV*	EATGK V* S-K*	UASCENSION IN THE PROPERTY OF	380		•	•	•	•	•		
320	— P.	LDEETA	INVRNLPASQ KPLGSINR	SUKPLNSKGK URSGRONS	370	•	•	SSVKKMH*	•	1	•		•
310	7 0	-SIMEOKIAE TILMEKRIAE		TAT XADAITAE.	360	 - -		SNITHINEG					
	301 301 301	301	301	30T		351	351	351	351	351	351	351	351
	Human LPAAT-β Human LPAAT-α Yeast LPAAT	E.coli LPAAT H.influenzae	S.typhimuriu L.douglassi	C. nucitera		Human L.PAAT-B	Human L.P.AATa	Yeast LPAAT	E.coli L.PAAT	H. influenzae	S. typhimuriu	L.douglassi	C. nucifera

Figure 9 A

_															
תרת	ATGA	AACC	AACA	TACA	TGGC	STTTC	CATO	CACAG	TTGG	AGTC	AGAT	GTGA	'CCC	GGAG	60
	555 6	CTCT	CCCT	ጥርጥር	CACCO	CGGA	AGCCC	TGAC	JGGCA	rec 10	LLLCC	CACI	アンシン	CIGC	120
		\sim TCC		ころして	ഭഗസഭം	רכדנ	~AGCC	JAGGC		TUCA	c	CICC	. I GAG	CAGC	180
<u> </u>	3000	GGC	CTG	CTG	GCC	TTC	CTG	AAG	ACC	CAG	TTC	GIG	CIG	CAC	225
	Met	Gly	Leu	Leu	Ala 5	Phe	Leu	Lys	THE	10	rne	Val	Leu	UIS	
CTG	CTG	GTC	GGC	TTT	GTC	TTC	GTG	GTG	AGT	GGT	CTG	GTC	ATC	AAC	270
T.AT	Leu	Val	Gly	Phe	Val	Phe	Val	Val	Ser	Gly	Leu	Val	Ile	Asn	
9.5					20					25					
		CAG	CTG	TGC	ACG	CTG	GCG	CTC	TGG	CCG	GTC	AGC	AAG	CAG	315
Phe	Val	Gln	Leu	Cys	Thr	Leu	Ala	Leu	Trp	PIO	Val	Ser	Lys	Gln	
					35					40					360
CTC	TAC	CGC	CGC	CTC	AAC	TGC	CGC	CTC	GCA 31a	TAC	FOT	Lac	TGG	AGC Sor	300
Lev	TYI	Arg	Arg	Leu	Asn	Cys	Arg	Leu	Ala	55	Ser	neu	тър	Ser	
45	; \ CTG			000	50	CAC	TCC	TGG	ጥርር		ACG	GAG	TGT	ACA	405
CAA	CTG Leu	GTC	ATG	CIG	CIG	GAG	Trn	ጥተው	Ser	Cvs	Thr	Glu	Cvs	Thr	
		var	mec	rea	65	GIG				70					•
60		ACG	GAC	CAG	GCC	ACG	GTA	GAG	CGC	TTT	GGG	AAG	GAG	CAC	450
CTC	. Phe	Thr	Asp	Gln	Ala	Thr	Val	Glu	Arg	Phe	Gly	Lys	Glu	His	
					80					83					
		ATC	ATC	CTC	AAC	CAC	AAC	TTC	GAG	ATC	GAC	TTC	CTC	TGT	495
Ala	Val	Ile	Ile	Leu	Asn	His	Asn	Phe	GIU	TIE	Asp	Phe	Leu	Cys	
					95					LUU					540
GGC	TGG	ACC	ATG	TGT	GAG	CGC	TTC	Clar	Un I	Len	Gly	Ser	Ser	Lve	340
	Trp	Thr	Met	Cys	GIU	Arg	Pne	GIY	VAI	115	Gly	JEI	Jei	د رد	
105	S CTC	COM	220	AAG	110	СТС	CTC	TAC	GTG		CTC	ATC	GGC	TGG	585
GTO	CTC L Leu	815	Tare	LVS	Glu	Leu	Leu	Tyr	Val	Pro	Leu	Ile	Gly	Trp	
					125					720					
120		TAC	TTT	CTG	GAG	ATT	GTG	TTC	TGC	AAG	CGG	AAG	TGG	GAG	630
The	Trp	Tyr	Phe	Leu	Glu	Ile	Val	Phe	Cys	Lys	Arg	Lys	Trp	Glu	
	_				7 4 ()					747					675
GAG	5 G GAC	CGG	' GAC	ACC	GTG	GTC	GAA	GGG	CTG	AGG 7×4	3-70	Lav	Sor	ACD	675
Gli	1 Asp	Arg	Asp	Thr	Val	Val	GIU	GIY	rea	160	ALG	nec	Ser	Asp	
150	o C CCC				155	COLTAN	CTC	CTG	TAC			GGG	. ACG	CGC	720
TAC	c ccc	GAG	TAC	Mot	TGG	Phe	Leu	Leu	Tyr	Cvs	Glu	Gly	Thr	Arg	
	_				7 7 7 7 1 1					111					
169		GAG	ACC	AAG	CAC	CGC	GTT	AGC	ATG	GAG	GTG	GCG	GCI	GCT	765
TTV	. ACG	Glu	Thr	Lys	His	Arg	Val	Ser	Met	Glu	Val	Ala	a Ala	Ala	
	_				795					TJU	•				
		CTT	CCT	GTC	CTC	AAG	TAC	CAC	CTG	CTG	CCG	CGC	ACC	AAG	810
Lvs	Gly	Leu	Pro	Val	Leu	Lys	Tyr	His	Leu	nea	PLU	Arc	i uni	Lys	
	_				77 () ()					203					855
GG	TTC	ACC	ACC	GCA	GTC	AAG	TGC	CTC	7~~	Cly	· The	· Val	Als	GCT	623
Gly	Phe	Thr	Thr	Ala	Val	. Lys	Cys	rea	YT. A	220	1111	Val	LALC	Ala	
210	כ				215	220	ጥጥር	AGA	GGA	AAC	AAC	: AAC	CCC	TCC	900
GT	TAT	GAT	GTA	ACC	CiG	AAC	Dhe	Ara	Glv	Asn	Lvs	Ası	1 Pro	Ser	-
		Asp	Val	THE	230	Vall	2 110	*** 3	1	235					•
225	5		N TO C	CTC	TAC	GGG	AAG	AAG	TAC	GAG	GCG	GAC	C ATC	TGC	945
CTC	CIG	C114	TIO	Len	Tvr	Glv	Lvs	Lys	Tyr	Glu	Ala	Asp	Met	Cys	
					745					230					
240		AGA	Lalah	ССТ	CTG	GAA	GAC	ATC	CCG	CTG	GAT	GA	A. AAC	GAA	990
17n 1	Ara	Ara	Phe	Pro	Leu	Glu	Asp	Ile	Pro	Den	voř	Glu	ı Lys	Glu	
					260					203)				
GC	GCT	CAG	TGG	CTT	CAT	AAA	CTG	TAC	CAG	GAG	AAG	GAC	GCC	CTC	1035

Figure 9 B

Ala	Ala	Gln	Trp	Leu	His 275	Lys	Leu	Tyr	Gln	Glu 280	Lys	Asp	Ala	Leu	
270	GAG	ልጥል	ТАТ	AAT		AAG	GGC	ATG	TTT	CCA	GGG	GAG	CAG	TTT	1080
CAG	GAG Glu	Ile	Tyr	Asn	Gln	Lys	Gly	Met	Phe		Gly	Glu	GIn	Phe	
285			_		290			cmc	CEC	295	ጥጥር	CTG	TCC	TGG	1125
AAG	CCT	GCC	CGG	AGG	CCG	TGG	ACC	Lau	Len	Acn	Phe	Leu	Ser	Trp	
Lys	CCT Pro	Ala	Arg	Arg	305	Trp	TILL	Dea	Deu	310				_	
300	ACC	* WW	CTC.	СТС	mcm.	CCC	CTC	TTC	AGT	TTT	GTC	TTG	GGC	GTC	1170
_	ACC	Tle	Leu	Leu	Ser	Pro	Leu	Phe	Ser	FILE	Val	Leu	Gly	Val	
Ala 315															1215
TTT	GCC	AGC	GGA	TCA	CCT	CTC	CTG	ATC	CTG	ACT	TTC	Len	Glv	TTT Phe	1413
Phe	Ala	Ser	Gly	Ser	Pro	Leu	ren	116	Dea	340					
330		CCA	CCT	ጥርር	335 TTT	GGA	GTT	CGC	AGA	CTG	ATA	GGA	GTA	ACT Thr	1260
GTG	GGA	Ala	Ala	Ser	Phe	Gly	Val	Arg	Arg	200		Gly	Val	Thr	
															1305
GAG	ATA	GAA	AAA	GGC	TCC	AGC	TAC	GGA	AAC	CAA	GAG	Phe	LVS	AAA Lvs	1303
Glu	Ile	Glu	Lys	Gly	Ser	Ser	TAT	GIY	A514	370					
360		ma a	מיתים	a ጥርር	COCT	GACT	GAAC	ACAC	GCGG	CCCI	GAC	GTGC	TATO	CAGTT	1362
AAG	GAA	***	112	A100		••••									1422
PAC	TCAA	AACC.	AACA	CACA	GAGT	GCAG	GAAA	AGAC	TTAA	AGA		יא א כיני יא א כיני	.TCT.	TATTAA TCAGG	1482
CTG	GTGA	CTAA	TATT.	AACA	AAAC	TTGA		CCAC	ጉሌያ	TCC	ACGC	CGC	CGT	GGAGG	1542
															1602
TGG	GTCC CCTT	GGCC	GGAG TCCT	ሊሁሁር ጥጥርጥ	CTCC	AATT	ACTI	AGAT	CAA	\TTT	LAAAT	LAAA	LAAA	AAAA	1660
GGA	CCTT	1000													

Figure 10 A

TACT	CAC	rCTG ccc	これここ	TAGO	CACA!	AAACI	YAGAA	IGGCC IGGCC	ATCA	AGCA TGGA	GAGC	CTTC	ATCT	TCGCC GACT TGCC CTG Leu	61 121 181 238
CTG Leu	GAG Glu	Trp	TGG Trp	TCC Ser	TGC Cys	ACG Thr	GAG Glu 10	TGT Cys	ACA Thr	CTG Leu	TTC Phe	ACG Thr 15	GAC Asp	CAG Gln	283
GCC	ACG Thr	5 GTA Val	GAG Glu	CGC Arg	TTT Phe	GGG Gly	AAG	GAG Glu	CAC His	GCA Ala	GTC Val	ATC Ile	ATC Ile	CTC Leu	328
	C) C	20	TTC Phe	GAG	АТС	GAC	TTC	CTC	TGT	GGG	TGG	ACC	ATG	TGT	373
	000	35	GG A	GTG.	CTG	GGG	AGC	TCC	AAG	GTC	CTC	GCT	AAG	AAG	418
Glu	Arg	Phe 50	Gly	Val	Leu	Gly	Ser 55	GGC	TGG	ACG	TGG	60 TAC	TTT	CTG	463
Glu	Leu	Leu	Tyr	Val	Pro	Leu	70	GIA	Trp	THE	тър	75	Pile	pen	500
Glu	Ile	Val	TTC Phe	Cys	Lys	Arg	ւչs 85	Trp	GIU	GIU	ASP	90	vab	TILL	508
GTG Val	GTC Val	GAA Glu	GGG Gly	CTG Leu	AGG Arg	CGC Arg	Leu	TCG Ser	GAC Asp	TAC Tyr	CCC Pro	GAG Glu 105	TAT	ATG Met	553
TGG	TTT	95 CTC Leu	CTG Leu	TAC Tyr	TGC Cys	GAG Glu	GGG Gly	ACG Thr	CGC	TTC Phe	ACG Thr	GAG Glu	ACC Thr	AAG Lys	598
		110	3.00	አ መረግ	GNG	CTC	CCC	GCT	GCT	AAG	GGG	CTT	CCT	GTC Val	. 643
_		125	C3.C	CITIC	CTG	cce	CCC	ACC	AAG	GGC	TTC	ACC	ACC	GCA	688
Leu	Lys	Tyr 140	His	Leu	Leu	Pro	145	GCA	GCT	GTC	TAT	150 GAT	GTA	ACC	733
Val	Lys	Cys	Leu	Arg	GIA	Thr	160	Ala	ATG	val	ıyı	165	, ,		778
Leu	Asn	Phe	Arg	Gly	Asn	Lys	175	Pro	Ser	Leu	Deu	180)	CTC Leu	770
TAC Tyr	GGG Gly	_	AAG Lys	TAC Tyr	GAG Glu	GCG Ala	ASD	mec	TGC Cys	GTG Val	AGG	AGA Arg 199	, Elle	CCT Pro	823
		185	3.000	CCC	CTC	CAT	CZZ	AAG	GAA	GCA	GCI	CAC	TGC	CTT Leu	868
•		200	ma C	CNG	GAG	AAG	GAC	GCG	CTC	CAG	GAG	AT	A TAS	TAA 7	913
His	Lys	215	Tyr	GIN	CCA	гуs	220 GAG	CAG	TTT	AAG	CCI	22! GC	5 C CG(AGG	
Gln	Lys	Gly	Met	Phe	Pro	GIĀ	235	GIN	Pne	Lys	PLC	240)	, ALG	
CCG Pro	Trp	ACC Thr	CTC Leu	CTG Leu	AAC Asn	TTC Phe	CTG Leu 250	ser	TGG Trp	GCC Ala	ACC	: AT' : Il	- 50	C CTG	1003
TCT Ser		245 CTC Leu	TTC Phe	AGT Ser	TTT Phe	GTC Val	TTG	GGC	GTC Val	TTT Phe	GCC	: AG	GGZ	A TCA Y Ser	1048

Figure 10 B

.17		260					265					270			
CCT	CTC	CTG	ATC	CTG	ACT	TTC	TTG	GGG	TTT	GTG	GGA	GCA	GCT	TCC	1093
CCI		T All	Tle	1.011	Thr	Phe	Leu	Glv	Phe	Val	Gly	Ala	Ala	Ser	
Pro	Leu		116	DCG	+		280				-	285			
		275						CER	N CIT	CAC	ስ ጥስ		222	CCC	1138
TTT	GGA	GTT	CGC	AGA	CTG	ATA	GGA	GTA	ACI	GAG	210	CAA	~~~	930	1130
Phe	Glv	Val	Arg	Arg	Leu	Ile	Gly	Val	Thr	GIU	TIE	GIU	гλг	GIY	
	_	290					295					300			
mac	NCC	TAC	GGA	AAC	CAA	GAG	TTT	AAG	AAA	AAG	GAA	TAA	TTA	ATGGC	1185
1.00	AGC	m.~	Gly	Acn	Gln	Glu	Phe	Lys	Lvs	Lvs	Glu	***			
Ser	Ser		'GTĀ	VOII	GIII	0.10	310	-1-	-4-						
		305							- 2 CM	TI N N C	מ מ מישת			~~~~	1245
TGT	SACTO	JAAC /	ACACO	CGG	CCTC	SACGO	a'I'GG'	LATC	AGI.	IAAC	ICAM		MACA!	CACAG	1245
» CTC	CAGO	AAA.	AGACA	ATTA	AGAA	CTA	CTTTC	CTT	ATTA	ACTG	GTGA	CT'AA'	TATT.	AACAA	1305
	nmc 2 (CCA	CAGI	א א אח	CTAAF	rcag?	\AGG(CTG	rcag(GTGA.	AGTC'	LICA	GCCT	CCCAC	1365
AAC	LIGA	3CC12	CACC	יא חיריי	PCC AC	CCGC	יפרכנ	CTGC	GAG	GTGG	GTCC	GCC	GGAG.	AGGCC	1425
AGC	CAG	٠٠١٠٠	CAGC	.n.c.		A COC			ACA	CCCA	اللملات	TGGC	ጥርርጥ	TTCTC	1485
TCC		SACGO	CGLC	TCT	CAGA	44C1		1 2 2 2 3	2.37						1523
TCC	LAATT	\CTT	GATO	CAAA	rttt?	VAAA	\AAAA	LAAA	AAA						1525
		•													

Figure 11A

Figur															
TGAAC	CCA	GCCGC	CTCC	ATCI	CAGO	TTCT	GGTI	TCTA	AGTC	CATG	TGCC	AAAG	GCTG	CCAG	61
		~~~~	DMCC	ירים אירייי	יררתנ	CATIC	1.1.1.	. 1		SOM	$\alpha r c r$	TIGN		<del>UUU</del>	121
TAGT	TTAT	TATT	CTG	<u>LATA</u>	GAGC	GTCC	ACGC	ATC	AIG	GAC	CIC	GCG	GGA	CIG	175
									met	ASP	Leu	Ala	Gly	Leu	
		mam	CAC	mm/C	CTC	TCC	CAC	CTG	GTC	TTC	TGC	TAC	GTC	TTT	220
CTG	AAG	Sor	CAG	Phe	Leu	Cvs	His	Leu	Val	Phe	Cys	Tyr	Val	Phe	
	_		10					TD					20		
АТТ	GCC	TCA	CCC	CTA	ATC	ATC	AAC	ACC	TTA	CAG	CTC	TTC	ACT	CTC	265
Ile	Ala	Ser	Gly	Leu	Ile	Ile	Asn	THE	Ile	Gln	Leu	Phe	THE	Leu	
			25				CAC	30	ጥጥር	CGG	AAG	ልጥር	35	TICC	310
CTC	CTC	TGG	CCC	ATT	AAC	LVS	Gln	Leu	Phe	Arg	Lvs	Ile	AAC Asn	Cvs	310
			40					45					50		
AGA	CTG	TCC	መእጥ	TGC	ATC	TCA	AGC	CAG	CTG	GTG	ATG	CTG	CTG	GAG	355
Arg	Leu	Ser	Tyr	Cys	Ile	Ser	Ser	GIN	Leu	Val	Met	Leu	rea	Glu	
			55					00					65		400
TGG	TGG	TCG	GGC	ACG	GAA	TGC	Thr	Tle	Phe	Thr	Asp	Pro	CGC Arg	Ala	400
			70					12					90		
ጥልሮ	CTC	AAG	mam.	GGG	AAG	GAA	AAT	GCC	ATC	GTG	GTT	CTC	AAC	CAC	445
Tyr	Leu	Lys	Tyr.	Gly	Lys	Glu	Asn	Ala	Ile	Val	Val	Leu	Asn	His	
_			. 0 5					. 30					77		490
AAG	TTT	GAA	ATT	GAC	J.I.I.	Len	CVS	Gly	Trp	Ser	Leu	Ser	GAA Glu	Arg	
-			100					TOD					770		
TTT	GGG	CTG	COCT A	GGG	GGC	TCC	AAG	GTC	CTG	GCC	AAG	AAA	GAG	CTG	535
Phe	Gly	Leu	Leu	Gly	Gly	Ser	Lys	Val 120	Leu	Ala	Lys	Lys	Glu 125	Leu	
			115	3 (1)(1)	አጥር	GGC	. TGG	ATG	TGG	TAC	TTC	ACC	GAG	ATG	580
GCC	TAT	GTC V=1	Pro	Tle	Tle	Glv	Trp	Met	Trp	Tyr	Phe	Thr	Glu	Met	
			120					כנג					740		
GTC	TTC	TGT	TCG	CGC	AAG	TGG	GAG	CAG	GAT	CGC	AAG	ACG	GTT	GCC	625
Val	Phe	Cys	Ser	Arg	Lys	Trp	Glu	150	Asp	Arg	Lys	Thr	155	ATA	
			145	CAC	CTC	cee	GAC	TAC	ccc	GAG	AAG	TAT	TTT	TTC	670
ACC	AGT	Leu	Gln	His	Leu	Arg	Asp	Tyr	Pro	Glu	Lys	Tyr	Phe	Phe	
			160					103					1/0		
CŤG	ATT	CAC	TGT	GAG	GGC	ACA	CGG	TTC	ACG	GAG	AAC	AAC	CAT	GAG	715
Leu	Ile	His	Cys	Glu	Gly	Thr	Arg	180	TILL	GIU	rrys	r.Y.	185	GIU	
		100	175	CTC	ccċ	cee	GCC	AAG	GGG	CTC	CCI	CGC	CTC	AAG	760
ATC	AGC	Mot	Gln	Val	Ala	Arg	Ala	Lys	Gly	Let	ı Pro	Arg	у гес	r raz	
CAT	CAC	CTG	mmc	CCA	CGA	ACC	AAG	GGC	TTC	GCC	TA	ACC	GTO	AGG	805
His	His	Leu	Leu	Pro	Arg	Thr	Lys	210	Pile	. ATS	1 116	e Thi	219	. Arg	
			205	cm.	·	тс»	CCT	GTA	TAT	' GAC	TGT	. AC	A CTC	AAT	850
AGC	TTG	AGA	AAT	Unl	Val	Ser	Ala	Val	Туг	Ası	Cys	Th	r Lei	ı Asn	
			220										231	,	
ጥጥሮ	AGA	ААТ	3 3 M	GAA	AAT	CCA	ACA	CTG	CTG	GG	A GTO	CT	A AAC	GGA	895
Phe	Arg	Asn	Asn	Glu	Asn	Pro	Thr	Leu	. Let	Gl	/ Val	Le	T W21	1 GIA	
			226					240					<b>44</b> .	3	
AAG	AAA	TAC	CAT	GCA	GAT	TIG	TAT	Val	Aro	Arc	J Tla	Pro	n CIC	GAA Glu	. Jau
CAC	አ ጥC	ССТ	033	GAC	GAT	GAC	GAG	TGC	TCC	GC	TGG	CT	G CAC	AAG	985
Aen	Tle	Pro	Glu	Asp	Asp	Asp	Glu	CAP	261	Ala	a Tri	Le	n ur:	a raa	
vab			265					270					279	5	

#### Figure 11B

CTC	TAC	CAG	GAG	AAG	GAT	GCC	TTT	CAG	GAG	GAG	TAC	TAC	AGG	ACG	1030
TAN	TVY	Gln	Glu	Lys	Asp	Ala	Phe	Gln	Glu	Glu	Tyr	Tyr	AIG	Thr	
			280					285					290		
GGC	ACC	TTC	CCA	GAG	ACG	CCC	ATG	GTG	CCC	CCC	CGG	CGG	CCC	TGG	1075
GIV	Thr	Phe	Pro	Glu	Thr	Pro	Met	Val	Pro	Pro	Arg	Arg	PIO	Trp	
			295					300					305		
ACC	CTC	GTG	AAC	TGG	CTG	TTT	TGG	GCC	TCG	CTG	GTG	CTC	TAC	CCT	1120
Thr	Leu	Val	Asn	Trp	Leu	Phe	Trp	Ala	Ser	Leu	Val	Leu	JÄI	Pro	
			310					315					320		
TTC	TTC	CAG	TTC	CTG	GTC	AGC	ATG	ATC	AGG	AGC	GGG	TCT		CTG	1165
Phe	Phe	Gln	Phe	Leu	Val	Ser	Met	Ile	Arg	Ser	GTÅ	Ser	335	Leu	
			325					330		cma	000	mcc.		CCA	1210
ACG	CTG	GCC	AGC	TTC	ATC	CTC	GTC	TTC	J-I-I.	616	313	TCC	Val	GUA	1210
Thr	Leu	Ala	Ser	Phe	IIe	Leu	val	345	Pne	var	ATG	SET	350	GLY	
		TGG	340	3 000	CCM	CTC	) CG		שייי ע	GAC	AAG	GGC		GCC	1255
GTT	CGA	TGG	ATG	TIO	Clas	77=1	Thr	Glu	Tle	Asp	Lvs	Glv	Ser		366
Val	Arg	Trp	355	TIE	GLY	Val	1111	360			-1-	3	365		
	000	AAC	ጥርጥ	GAC	AGC	AAG	CAG	AAA	CTG	AAT	GAC	TGA	CTC	AGGG	1301
TAC	C1.	Asn	Ser	Asp	Ser	Lvs	Gln	Lys	Leu	Asn	Asp	***			
_			ママハ					375							
AGGT	этсас	CAT	CGA	AGGG	AACC	TTGG	GGAA	CTGG'	TGGC	CTCT	GCAT	ATCC	TCCT	TAGT	1361
		-m- 7 (	אם ממר	こここででく	ാരവാ	こみにつ	ጉርርጥ	SCTG	GGCA	CGGC	GGAA	GICA	CGAC	CICI	1421
		~~ x <b>~</b> ?	ኮሮሞርር	こかしかく	つみならの	CCG	SATG	GGGA(	GGAA	GATG	.IIII.	GIAA	$T_{c}T_{c}T_{c}T_{c}T_{c}T_{c}T_{c}T_{c}$	T.T.T.T.	1481 1541
			ריתי א כיני	raca	ንጥጥጥ	بلبلت	ייירטיייו	$T^{\mu}T^{\nu}T^{\nu}T^{\nu}$	GTGC	GAGT	GIGI	GIGH	CANI	GGCT.	1601
GTGT	3GTG2	AGTG	rgaac	CTTTC	STTC'	TGTG	ATCA'	TAGA	AAGG	CTAT	LT.T.Y	. T. D. D. D.	CACT	GGGA	1661
GGGC	AGGG	CTGG	GAC	CGAA	3GGG/	ACAA	21.I.C		Cuuuu	JCCT	CACA	TCAC	מ ב בידי	ጥጥልጥ	1721
TGTA	ACCC'	rtgg'	TGCC	LAGA	シムエム	ひこしむ	ישאראני ישאראני	MG I.G.	$\Delta \Delta \nabla \nabla$	AAAA	AAAA	AAAA	A	TATT	1774
GCCT	CCAA	SAAA	<b>WAAA</b>	777.1.1.7	WW.	1001	1110	1000	TCAA						